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SEQUENCE LISTING

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<120> Helicobacter pylori live vaccine

<130> 100564-09008

<140> 09/284,233

<141> 1999-07-28

<150> PCT/EP97/04744

<151> 1997-09-01

<150> EP/96 116 337.5

<151> 1996-10-11

<160> 9

<170> PatentIn version 3.0

<210> 1

<211> 1557

<212> DNA

<213> Helicobacter pylori

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<221> CDS

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 Met Thr Phe Gly Tyr Glu Leu Gly Gln Val Val Gln Gln Val Lys Asn
 35 40 45
 ccg ggt aaa atc aaa gcc gaa gaa tta gcc ggc ttg tta aac tct acc
 Pro Gly Lys Ile Lys Ala Glu Glu Leu Ala Gly Leu Leu Asn Ser Thr
 50 55 60
 aca aca aac aac acc aat atc aat att gca ggc aca gga ggc aat gtc
 Thr Thr Asn Asn Thr Asn Ile Asn Ile Ala Gly Thr Gly Gly Asn Val
 65 70 75 80
 gcc ggg act ttg ggc aac ctt ttt atg aac caa tta ggc aat ttg att
 Ala Gly Thr Leu Gly Asn Leu Phe Met Asn Gln Leu Gly Asn Leu Ile
 85 90 95
 gat ttg tat ccc act ttg aac act agt aat atc aca caa tgt ggc act
 Asp Leu Tyr Pro Thr Leu Asn Thr Ser Asn Ile Thr Gln Cys Gly Thr
 100 105 110
 act aat agt ggt agt agt agt ggt ggt ggt gct gcc aca gcc gct
 Thr Asn Ser Gly Ser Ser Ser Gly Gly Ala Ala Thr Ala Ala
 115 120 125
 gct act act agc aat aag cct tgt ttc caa ggt aac ctg gat ctt tat
 Ala Thr Thr Ser Asn Lys Pro Cys Phe Gln Gly Asn Leu Asp Leu Tyr
 130 135 140
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 Arg Lys Met Val Asp Ser Ile Lys Thr Leu Ser Gln Asn Ile Ser Lys
 145 150 155 160
 aat atc ttt caa ggc aac aac acc acg agc caa aat ctc tcc aac
 Asn Ile Phe Gln Gly Asn Asn Thr Thr Ser Gln Asn Leu Ser Asn
 165 170 175
 cag ctc agt gag ctt aac acc gct agc gtt tat ttg act tac atg aac
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 180 185 190
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 195 200 205

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245	250	255	
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275	280	285	
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Gly Val Gly Asn Gly Pro Thr Tyr Asn Gln Val Asn Leu Leu Thr Tyr			
385	390	395	400
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Gly Val Gly Thr Asp Val Leu Tyr Asn Val Phe Ser Arg Ser Phe Gly			
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Ser Arg Ser Leu Asn Ala Gly Phe Phe Gly Gly Ile Gln Leu Ala Gly			
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435	440	445	

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Pro Thr Ala Thr Lys Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met	
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Asn Phe Gly Ile Leu Lys Lys Asp Leu Lys Ser His Asn Gln His Ser	
465 470 475 480	
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Ile Glu Ile Gly Val Gln Ile Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys	
485 490 495	
gct ggc ggt gct gaa gtg aaa tac ttc cgc cct tat agc gtg tat tgg	1536
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115 120 125

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130 135 140

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290 295 300

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Trp Leu Gly Asn Phe Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe
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420 425 430

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Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr			
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cag ctc ggg caa gtc atg caa gat gtc caa aac cca ggc ggc gct aaa			144
Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala Lys			
35 40 45			
agc gac gaa ctc gcc aga gag ctt aac gct gat gta acg aac aac att			192
Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn Ile			
50 55 60			
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Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn Ala			
65 70 75 80			
ttc tcc caa tac ctt tat tcg ctt tta ggg gct tac ccc aca aaa ctc			288
Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys Leu			
85 90 95			
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Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val Gly			
100 105 110			
tct ggg act tgt gcg gct gca ggg acg gct ggt ggc act tct ctt aac			384
Ser Gly Thr Cys Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu Asn			
115 120 125			
act caa agc act tgc acc gtt gcg ggc tat tac tgg ctc cct agc ttg			432
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130 135 140			
act gac agg att tta agc acg atc ggc agc cag act aac tac ggc acg			480
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165 170 175			
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Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu Glu Asn Lys Asn			
180 185 190			
gga act agt gct agt gga act agt ggt gcg act ggt tca gat ggt			624
Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp Gly			
195 200 205			
caa act tac tcc aca caa gct atc caa tac ctt caa ggc caa caa aat			672
Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln Asn			
210 215 220			

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ggg act gat gtg ttg tat aac atc ttt agc cgc tcc tat caa aac cgc Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg 405 410 415	1248
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50 55 60

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Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys Leu
85 90 95

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100 105 110

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115 120 125

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130 135 140

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145 150 155 160

Asn Thr Asn Phe Pro Asn Met Gln Gln Leu Thr Tyr Leu Asn Ala
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195 200 205

Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln Asn
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Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu Leu
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245 250 255

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Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser Ala
275 280 285

Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln Gly
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Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr Leu
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Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr Leu
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Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn
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Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg
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Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr
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Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys
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 tttaacttta agaaggagat atacat atg aaa ctg act ccc aaa gag tta gac 593
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aag ttg atg ctc cac tac gct gga gaa ttg gct aaa aaa cgc aaa gaa 641
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